



Comparative Metagenomics of Microbial Communities from Pristine and Contaminated Groundwater

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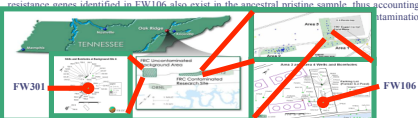


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INTRODUCTION

Research community. DOE, Joint Genome Institute, Walnut Creek, CA; ⁶Lawrence Berkeley National Laboratory, Berkeley, CA; ⁷Lawrence Livermore National Laboratory, Livermore, CA; ⁸Department of Microbiology, Michigan State University, East Lansing, MI

Research Center (FRC) has recently been analyzed to determine the effects of multiple stressors on microbial community structure. The sample was obtained from a site (FW106) experiencing long-term (>50 yrs) exposure to high concentrations of uranium, nitric acid and organic solvents. Analysis indicates a very low diversity community dominated by denitrifying γ - and β -proteobacteria. Furthermore, metabolic reconstruction reveals adaptations for specific geochemical parameters including: denitrification pathways; pathways for degradation of organic molecules including 1,2-dichloroethane, acetone, butanol, methanol and formaldehyde; a large variety of heavy metal resistance systems (cysABC, cysD, cadA, merA/CPI, etc.). Furthermore, many of these adaptations appear to be the result of lateral gene transfer. Abundance profiles of FW106 compared to all sequenced bacterial isolates show that several geochemically-relevant transporter genes, including *narK* nitrate/nitrite antiporter and *cysABC* and *cysD* divalent cation efflux, have been accumulated in the FW106 community. Comparisons of FW106 to the acid mine drainage community metagenome reveals community-specific gene profiles (e.g. geochemical genes, cytochromes, etc.) but also common mechanisms of adaptation, including the accumulation of *cysABC* metal transporter genes. Finally, the FW106 metagenome was compared to the preliminary (100 Mb) metagenomic sequence from pristine FRC groundwater (FW301). In contrast to the low species diversity of FW106, FW301 is represented by multiple phyla (predicted 400+ species) including α -, β -, and γ -proteobacteria, Planctomycetes, Chloriflexi, Actinobacteria, Acidobacteria and Firmicutes. In contrast to the FW106 sample which yields large contigs, the FW301 sample is composed largely of single reads that do not assemble into contigs (95%). Most of the geochemical resistance genes identified in FW106 also exist in the ancestral pristine sample, thus accounting for contamination.



FW106 Groundwater Geochemistry

Parameter	FW106	FW301
Uranium (mg/L)	1.5	2.3
Nitrate (mg/L)	1.5	2.3
Acetone (mg/L)	1.5	2.3
Butanol (mg/L)	1.5	2.3
Methanol (mg/L)	1.5	2.3
Formaldehyde (mg/L)	1.5	2.3
Acetate (mg/L)	1.5	2.3
Butyrate (mg/L)	1.5	2.3
Formate (mg/L)	1.5	2.3
Pyruvate (mg/L)	1.5	2.3
Lactate (mg/L)	1.5	2.3
Glucose (mg/L)	1.5	2.3
Fructose (mg/L)	1.5	2.3
Sucrose (mg/L)	1.5	2.3
Maltose (mg/L)	1.5	2.3
Starch (mg/L)	1.5	2.3
Cellulose (mg/L)	1.5	2.3
Chitin (mg/L)	1.5	2.3
Chitosan (mg/L)	1.5	2.3
Protein (mg/L)	1.5	2.3
Ammonia (mg/L)	1.5	2.3
Nitrite (mg/L)	1.5	2.3
Nitrogen (mg/L)	1.5	2.3
Phosphate (mg/L)	1.5	2.3
Sulfate (mg/L)	1.5	2.3
Sulfide (mg/L)	1.5	2.3
Iron (mg/L)	1.5	2.3
Copper (mg/L)	1.5	2.3
Zinc (mg/L)	1.5	2.3
Lead (mg/L)	1.5	2.3
Cadmium (mg/L)	1.5	2.3
Mercury (mg/L)	1.5	2.3
Chromium (mg/L)	1.5	2.3
Manganese (mg/L)	1.5	2.3
Cobalt (mg/L)	1.5	2.3
Nickel (mg/L)	1.5	2.3
Silver (mg/L)	1.5	2.3
Gold (mg/L)	1.5	2.3
Platinum (mg/L)	1.5	2.3
Palladium (mg/L)	1.5	2.3
Rhodium (mg/L)	1.5	2.3
Ruthenium (mg/L)	1.5	2.3
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Barium (mg/L)	1.5	2.3
Strontium (mg/L)	1.5	2.3
Calcium (mg/L)	1.5	2.3
Magnesium (mg/L)	1.5	2.3
Sodium (mg/L)	1.5	2.3
Potassium (mg/L)	1.5	2.3
Lithium (mg/L)	1.5	2.3
Boron (mg/L)	1.5	2.3
Fluorine (mg/L)	1.5	2.3
Chlorine (mg/L)	1.5	2.3
Bromine (mg/L)	1.5	2.3
Iodine (mg/L)	1.5	2.3
Selenium (mg/L)	1.5	2.3
Tellurium (mg/L)	1.5	2.3
Antimony (mg/L)	1.5	2.3
Bismuth (mg/L)	1.5	2.3
Vanadium (mg/L)	1.5	2.3
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